

Probes

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 13, 2001, 13:43:40 ; Search time 22.44 Seconds
(without alignments)
3107.164 Million cell updates/sec

Title: US-09-784-340-2
Perfect score: 527
Sequence: 1 MRSPKSLVYLLQLPFCVGC.....KCFIFSCQKFKTKIKRE 527

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 425026 seqs, 132305027 residues

Word size: 0

Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

- 1: SP-archaea:*
- 2: SP-bacteria:*
- 3: SP-fungi:*
- 4: SP-human:*
- 5: SP-invertebrate:*
- 6: SP-mammal:*
- 7: SP-mhc:*
- 8: SP-organelle:*
- 9: SP-phage:*
- 10: SP-plant:*
- 11: SP-rodent:*
- 12: SP-unclassified:*
- 13: SP-vertebrate:*
- 14: SP-virus:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	418	79.3	449	4 Q9H6S4	Q9H6S4 homo sapien
2	41	7.8	527	4 Q9Y4X1	Q9Y4X1 homo sapien
3	41	7.8	527	11 Q9ESE4	Q9ESE4 mus musculu
4	33	6.3	528	4 Q75614	Q75614 homo sapien
5	28	5.3	529	6 Q97951	Q97951 macaca fasc
6	28	5.3	529	6 Q9GLE0	Q9GLE0 macaca mula
7	27	5.1	529	6 Q9TSL6	Q9TSL6 macaca fasc
8	27	5.1	529	6 Q9GLD9	Q9GLD9 macaca mula
9	22	4.2	530	11 Q9R110	Q9R110 cavia porce
10	11	2.1	516	5 Q9XN3	Q9XN3 drosophila
11	11	2.1	516	5 Q9VGT0	Q9VGT0 drosophila
12	11	2.1	529	6 Q18736	Q18736 bos taurus
13	10	1.9	414	11 Q63662	Q63662 rattus norv
14	10	1.9	508	5 Q16276	Q16276 caenorhabd
15	10	1.9	530	11 P97886	P97886 rattus norv
16	10	1.9	531	5 Q21603	Q21603 caenorhabd
17	10	1.9	531	11 P70624	P70624 rattus norv
18	10	1.9	533	6 Q46423	Q46423 felis silve
19	10	1.9	533	6 Q46548	Q46548 felis silve

20	10	1.9	533	6 Q46549	Q46549 felis silve
21	9	1.7	135	4 Q9UHH3	Q9UHH3 homo sapien
22	9	1.7	434	2 Q9WZ99	Q9WZ99 thermotoga
23	9	1.7	509	14 Q91266	Q91266 spidoptera
24	9	1.7	515	14 Q73553	Q73553 spidoptera
25	9	1.7	530	4 Q14928	Q14928 homo sapien
26	9	1.7	530	4 Q00473	Q00473 homo sapien
27	9	1.7	530	4 Q00474	Q00474 homo sapien
28	9	1.7	530	4 Q06056	Q06056 homo sapien
29	9	1.7	530	4 Q9HAW9	Q9HAW9 homo sapien
30	9	1.7	530	4 Q9HAW7	Q9HAW7 homo sapien
31	9	1.7	530	4 Q18777	Q18777 oryctolagus
32	9	1.7	530	6 Q18777	Q18777 oryctolagus
33	9	1.7	530	6 Q9TSL8	Q9TSL8 macaca fasc
34	9	1.7	531	6 Q9XSS5	Q9XSS5 ovis aries
35	9	1.7	532	6 Q9XSS6	Q9XSS6 ovis aries
36	9	1.7	532	6 Q9TSL9	Q9TSL9 macaca fasc
37	9	1.7	533	6 Q9TSL7	Q9TSL7 macaca fasc
38	9	1.7	537	5 Q9XN4	Q9XN4 drosophila
39	9	1.7	537	5 Q9VGS9	Q9VGS9 drosophila
40	9	1.7	559	5 Q9VGT8	Q9VGT8 drosophila
41	9	1.5	17	11 Q9QUY6	Q9QUY6 rattus sp.
42	8	1.5	24	11 Q9QVE1	Q9QVE1 rattus sp.
43	8	1.5	215	4 Q9HCT7	Q9HCT7 homo sapien
44	8	1.5	284	4 Q9H3G2	Q9H3G2 homo sapien
45	8	1.5			

ALIGNMENTS

RESULT 1
ID Q9H6S4 PRELIMINARY: PRT: 449 AA.
AC Q9H6S4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE CDNA: FLJ21934 FIS, CLONE HEP04364.
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Ota T., Suzuki Y., Oabayashi M., Nishi T., Shibahara T.,
RA Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT "NEO human cDNA sequencing project";
RT Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK025587; BAB15179.1; -
SQ SEQUENCE 449 AA; 51390 MW; DA2E2B82C9FE1360 CRC64;

cannot use

Query Match	79.3%	Score 418;	DB 4;	Length 449;
Best Local Similarity	100.0%	Pred. No. 0;		
Matches 418;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 79	MPDDRRENEIFVDLALNVPLGSLTWSQVTKLNDFFVEIRGTLMKMCESFYNOTLTKKL 138			
DB 1	MPDDRRENEIFVDLALNVPLGSLTWSQVTKLNDFFVEIRGTLMKMCESFYNOTLTKKL 60			
QY 139	QETNYVMLIDPVIYPCGDLMAELLAVPEVLTIRISVGNERNRSCGKLPAPLSTVPPMTG 198			
DB 61	QETNYVMLIDPVIYPCGDLMAELLAVPEVLTIRISVGNERNRSCGKLPAPLSTVPPMTG 120			
QY 199	LTRDMTFLEKVKNSMLSVLFHFWIODYDHFHWEFPYSKALGRPTTLCETYGKAEIMLIRT 258			
DB 121	LTRDMTFLEKVKNSMLSVLFHFWIODYDHFHWEFPYSKALGRPTTLCETYGKAEIMLIRT 180			
QY 259	YMFEEFPOPYPNFEFVGLHCKPAKALPKEMENFVQSSGEGDIYVFSLSGLSQNTTEEK 318			
DB 181	YMFEEFPOPYPNFEFVGLHCKPAKALPKEMENFVQSSGEGDIYVFSLSGLSQNTTEEK 240			

QY 319 ANIASALAOIPQKYLWYKGGKSTLGANTPLYPWIPONDILGPKTKAFTTGGMNGI 378
|||||
DB 241 ANIISALAOIPQKYLWYKGGKSTLGANTPLYPWIPONDILGPKTKAFTTGGMNGI 300
QY 379 YEATYHGVPMVGPPIFGDOLNIAHMKAKGAVEINFKMTSEDLRLRYITDSSYKE 438
|||||
DB 301 YEATYHGVPMVGPPIFGDOLNIAHMKAKGAVEINFKMTSEDLRLRYITDSSYKE 360
QY 439 NAMRLSRHHQPVKPLDRAVFWIEFVNRHKGAKHLRSADLTWFOHYSIDVIGFLL 496
|||||
DB 361 NAMRLSRHHQPVKPLDRAVFWIEFVNRHKGAKHLRSADLTWFOHYSIDVIGFLL 418

RESULT 2
ID QY4X1 PRELIMINARY; PRT: 527 AA.
AC QY4X1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE UDP-GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
GN UGT2A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-OLFACTORY;
MEDLINE-99289328; PubMed-10359671;
RA Jeditlschky G.A., Cassidy A.J., Sales M., Pratt N., Burchell B.;
RT "Cloning and characterization of a novel human olfactory UDP-
glucuronosyltransferase."
RL Biochem. J 340:837-843(1999).
DR EMBL: AJ006054; CAB41974.1; -
InterPro: IPR002213; -
DR Pfam: PR00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
DR Transferase: Glycosyltransferase.
KW SEQUENCE 527 AA; 59872 MW; B99E73AA9A421F17 CRC64;
SQ

Query Match 7.8%; Score 41; DB 4; Length 527;
Best Local Similarity 100.0%; Pred. No. 5.6e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 435 SYKENAMRLSRHHQPVKPLDRAVFWIEFVNRHKGAKHLR 475
|||||
DB 435 SYKENAMRLSRHHQPVKPLDRAVFWIEFVNRHKGAKHLR 475

RESULT 3
ID Q9ESE4 PRELIMINARY; PRT: 527 AA.
AC Q9ESE4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OLFACTORY UDP-GLUCURONOSYLTRANSFERASE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BALE/C;
RA Heydel J.M.;
RT "Mus musculus mRNA for olfactory UDP-glucuronosyltransferase."
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF184901; AAC17003.1; -
Transferase
KW SEQUENCE 527 AA; 59878 MW; 136FB2A648F39C75 CRC64;
SQ

Query Match 7.8%; Score 41; DB 11; Length 527;
Best Local Similarity 100.0%; Pred. No. 5.6e-33;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 435 SYKENAMRLSRHHQPVKPLDRAVFWIEFVNRHKGAKHLR 475
|||||
DB 435 SYKENAMRLSRHHQPVKPLDRAVFWIEFVNRHKGAKHLR 475

RESULT 4
ID 075614 PRELIMINARY; PRT: 528 AA.
AC 075614;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DE UDP-GLUCURONOSYLTRANSFERASE 2B4 PRECURSOR.
GN UGT2B4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-93326164; PubMed-8333863;
RA Jin G.J., Miners J.O., Lillywhite K.J., Mackenzie P.I.;
RT "cDNA cloning and expression of two new members of the human liver
UDP-glucuronosyltransferase 2B subfamily."
RL Biochem. Biophys. Res. Commun. 194:496-503(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Mackenzie P.I.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF081793; AAC32272.1; -
InterPro: IPR002213; -
DR Pfam: PR00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
DR Transferase.
KW SEQUENCE 528 AA; 60497 MW; B6F5BA0705E952C4 CRC64;
SQ

Query Match 6.3%; Score 33; DB 4; Length 528;
Best Local Similarity 100.0%; Pred. No. 8.2e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 443 LSRHHQPVKPLDRAVFWIEFVNRHKGAKHLR 475
|||||
DB 443 LSRHHQPVKPLDRAVFWIEFVNRHKGAKHLR 475

RESULT 5
ID 097951 PRELIMINARY; PRT: 529 AA.
AC 097951;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE.
GN UGT2B18.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Beaulieu M., Levesque E., Barbier O., Turgeon D., Belanger G.,
Hum D.W., Belanger A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF016310; AAC98726.1; -
InterPro: IPR002213; -
SQ

DR Pfam: PF00201; UDPGT: 1.
 DR PROSITE: PS00375; UDPGT: 1.
 KM Transferase.
 SQ SEQUENCE 529 AA; 60801 MW; 3CECB497B8C3601F CRC64;

Query Match 5.3%; Score 28; DB 6; Length 529;
 Best Local Similarity 100.0%; Pred. No. 1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 448 HDQPKPLDRAVFWIEFVNRHKGAKHLR 475
 DB 450 HDQPKPLDRAVFWIEFVNRHKGAKHLR 477

RESULT 6
 O9GLE0 PRELIMINARY; PRT; 529 AA.
 AC O9GLE0;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE UGT2B9*2.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Dean B., Zhao S., King C.;
 RT "Nucleotide and Deduced Amino Acid Sequence of UGT2B9*2: a Novel UDP-
 RT Glucuronosyltransferase Isoform Cloned from Female Rhesus Monkey
 RT Liver.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF294901; AAG21377.1; -
 KM Transferase.
 SQ SEQUENCE 529 AA; 60831 MW; 1225A0163D9ADDF2 CRC64;

Query Match 5.3%; Score 28; DB 6; Length 529;
 Best Local Similarity 100.0%; Pred. No. 1e-19;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 448 HDQPKPLDRAVFWIEFVNRHKGAKHLR 475
 DB 450 HDQPKPLDRAVFWIEFVNRHKGAKHLR 477

RESULT 7
 O9TSL6 PRELIMINARY; PRT; 529 AA.
 AC O9TSL6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DT 01-JUN-2000 (TREMBlrel. 14, last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 2B23 PRECURSOR (EC 2.4.1.17).
 OS Macaca fascicularis (Craib eating macaque) (Cynomolgus monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20043918; PubMed=10579317;
 RA Barlier O., Levesque E., Belanger A., Hum D.W.;
 RT "UGT2B23, a novel uridine diphosphate-glucuronosyltransferase enzyme
 RT expressed in steroid target tissues that conjugates androgen and
 RT estrogen metabolites.";
 RL Endocrinology 140:5538-5548(1999).
 DR EMBL; AF112113; AAF14353.1; -
 DR InterPro; IPR002213; -

DR Pfam: PF00201; UDPGT: 1.
 DR PROSITE: PS00375; UDPGT: 1.
 KM Transferase: Glycosyltransferase.
 SQ SEQUENCE 529 AA; 60957 MW; 646315E6D970541A CRC64;

Query Match 5.1%; Score 27; DB 6; Length 529;
 Best Local Similarity 100.0%; Pred. No. 1.1e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 449 DQPKPLDRAVFWIEFVNRHKGAKHLR 475
 DB 451 DQPKPLDRAVFWIEFVNRHKGAKHLR 477

RESULT 8
 O9GLD9 PRELIMINARY; PRT; 529 AA.
 AC O9GLD9;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE UGT2B33.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecoidea; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Dean B., Zhao S., King C.;
 RT "Nucleotide and Deduced Amino Acid Sequence of UGT2B33: a Novel UDP-
 RT Glucuronosyltransferase Isoform Cloned from Female Rhesus Monkey
 RT Liver.";
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF294902; AAG21378.1; -
 KM Transferase.
 SQ SEQUENCE 529 AA; 60858 MW; B1956F947F1F78D6 CRC64;

Query Match 5.1%; Score 27; DB 6; Length 529;
 Best Local Similarity 100.0%; Pred. No. 1.1e-18;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 449 DQPKPLDRAVFWIEFVNRHKGAKHLR 475
 DB 451 DQPKPLDRAVFWIEFVNRHKGAKHLR 477

RESULT 9
 O9RI10 PRELIMINARY; PRT; 530 AA.
 AC O9RI10;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE UGT2A3.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriocognathi; Cavidae; Cavia.
 OX NCBI_TaxID=10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=HARTLEY; TISSUE=LIVER;
 RA Smith S.A., Nagalla S.R., Andrews D.P., Olsen G.D.;
 RT "Morphine regulation of a novel uridine diphosphate
 RT glucuronosyltransferase in guinea pig pups following in utero
 RT exposure.";
 RL Mol. Genet. Metab. 0:0-0(1999).
 DR EMBL; AF175221; AAD51732.1; -
 DR InterPro; IPR002213; -
 DR Pfam; PF00201; UDPGT: 1.

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DR PROSITE: PS00375; UDPGT: 1.
KW TRANSFERASE.
SQ SEQUENCE 530 AA; 59895 MW; EE2F394D3FD484E1 CRC64;

Query Match
Best Local Similarity 4.2%; Score 22; DB 11; Length 530;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 353 DWIPONDLLGHPRKRAFTTHGCG 374
DQ 356 DWIPONDLLGHPRKRAFTTHGCG 377

RESULT 10
ID Q9XYN3 PRELIMINARY; PRT; 516 AA.
AC Q9XYN3;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)
DE ANTENNAL-ENRICHED UDP-GLYCOSYLTRANSFERASE.
GN UGT35B OR CG6649.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CANTON S; TISSUE=ANTENNA;
RA Wang Q., Hasan G., Pikeleiny C.;
RT "Preferential Expression of Biotransformation Enzymes in the Olfactory
RT Organs of Drosophila melanogaster: the Antennae."
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF116554; AAD22027.1; -
DR FlyBase: FBgn0026314; Ugt35b.
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW TRANSFERASE.
SQ SEQUENCE 516 AA; 58355 MW; 930F894C224E96CA CRC64;

Query Match
Best Local Similarity 2.1%; Score 11; DB 5; Length 516;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GLTDRMTFLER 208
DQ 182 GLTDRMTFLER 192

RESULT 11
ID Q9VGT0 PRELIMINARY; PRT; 516 AA.
AC Q9VGT0;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2001 (TREMblrel. 16, Last annotation update)
DE UGT35B PROTEIN.
GN UGT35B OR CG6649.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxId=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Adams M.D., Cealniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Ananatisdes P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abell J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Botkova D., Botchan M.R., Bouck J., Brockstein P., Brothier P.,
RA Butkus K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostali M., Houston K.A., Howland T.J., Wei M.-H., Ileguam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kuip D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195 (2000).
DR EMBL: AE003690; AAF54595.1; -
DR FlyBase: FBgn0026314; Ugt35b.
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW TRANSFERASE.
SQ SEQUENCE 516 AA; 58321 MW; 87F821CFA36801C2 CRC64;

Query Match
Best Local Similarity 2.1%; Score 11; DB 5; Length 516;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 198 GLTDRMTFLER 208
DQ 182 GLTDRMTFLER 192

RESULT 12
ID O18736 PRELIMINARY; PRT; 529 AA.
AC O18736;
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE.
GN Bos taurus (Bovine).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NCBI_TaxId=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Yokota H.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB008677; BAA23359.1; -
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT: 1.

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DR PROSITE: PS00375; UDPGT: 1.
 KM Transferrase.
 SQ SEQUENCE 529 AA; 60678 MW; 10BEC0920A415F76 CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPR 366
 |||||
 DB 352 PONDLLGHPR 362

RESULT 13
 O63662 PRELIMINARY; PRT; 414 AA.
 AC O63662;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE RAT 3-METHYLCHOLANTHRENE-INDUCIBLE TRUNCATED UDP-
 DE GLUCURONOSYLTRANSFERASE.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90078234; PubMed=2512292;
 RT Iyanagi T., Matanabe T., Uchiyama Y.;
 RT "The 3-methylcholanthrene-inducible UDP-glucuronosyltransferase
 RT deficiency in the hyperbilirubinemic rat (Gunn rat) is caused by a -1
 RT frameshift mutation."
 RT J. Biol. Chem. 264:21302-21307(1989).
 DR EMBL: J05132; AAA42315.1; -;
 DR InterPro: IPR002213; -;
 DR Pfam: PF00201; UDPGT: 1.
 DR PROSITE: PS00375; UDPGT: 1.
 KW Transferrase.
 SQ SEQUENCE 414 AA; 46921 MW; 27E338829C0A92F4 CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPR 365
 |||||
 DB 353 PONDLLGHPR 362

RESULT 14
 O16276 PRELIMINARY; PRT; 508 AA.
 AC O16276;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE F39G3.1 PROTEIN.
 GN F39G3.1
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BRISTOL N2;
 RX MEDLINE=94150718; PubMed=7906398;
 RX Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
 RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
 RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
 RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,

RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
 RA Lightning J., Lloyd C., McMurtry A., Mortimore B., O'Callaghan M.,
 RA Parsons J., Percy C., Riken L., Roopra A., Saunders D., Showkhen R.,
 RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
 RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
 RA Watson A., Weinstock L., Wilkinson-Sproat J., Wohlman P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans."
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Du Z., Le T.T., Holmes A.;
 RN Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RL Submitted (Jul-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF016424; AMB5327.1; -;
 DR InterPro: IPR002213; -;
 DR Pfam: PF00201; UDPGT: 1.
 DR PROSITE: PS00375; UDPGT: UNKNOWN_1.
 SQ SEQUENCE 508 AA; 57185 MW; 5DD389CBFB99A7 CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 365 KTKAFITGCG 374
 |||||
 DB 345 KTKAFITGCG 354

RESULT 15
 P97886 PRELIMINARY; PRT; 530 AA.
 AC P97886;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE.
 GN UGT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MISTER;
 RX MEDLINE=97373506; PubMed=9271076;
 RA Iwano H., Yokota H., Ohgiya S., Yocumoto N., Yusa A.;
 RT "A critical amino acid residue, asp446, in UDP-
 RT glucuronosyltransferase."
 RL Biochem. J. 325:587-591(1997).
 DR EMBL: D83796; BAA18960.1; -;
 DR InterPro: IPR002213; -;
 DR Pfam: PF00201; UDPGT: 1.
 DR PROSITE: PS00375; UDPGT: 1.
 KW Transferrase.
 SQ SEQUENCE 530 AA; 60249 MW; F27423303EF3313 CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGHPR 365
 |||||
 DB 353 PONDLLGHPR 362

RESULT 16
Q21603 PRELIMINARY; PRT; 531 AA.
AC Q21603;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE M88.1 PROTEIN.
GN M88.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida; Rhabditoidea;
OC Rhabdilitidae; Pelodermidae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Sulston J.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins J., Kirsten J., Laister N., Johnston L.,
RA Jones M., Kershaw J., Murray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifkin L., Roopra A., Saunders D., Showkhen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K., Waterston R.,
RA Watson A., Wellstock L., Wilkinson-Spoat J., Woldman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: Z34802; CAA84336.1; -
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: UNKNOWN.1
SQ SEQUENCE 531 AA; 60249 MW; 156994087344D36E CRC64;

Query Match 1.9%; Score 10; DB 5; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 365 KTKAFITGG 374
DB 367 KTKAFITGG 376

RESULT 17
P70624 PRELIMINARY; PRT; 531 AA.
AC P70624;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE UGT1A7 (UDP-GLUCURONOSYLTRANSFERASE 1A7).
GN UGT1A7.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=FISHER;
RC Grove A.D., Kessler F.K., Metz R.P., Rittler J.K.;
RL J. Biol. Chem. 0:0-0(0).
RN [2]
RP SEQUENCE OF 1-150 FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY;
RC MEDLINE=97153116; PubMed=8999837;
RA Grove A.D., Kessler F.K., Metz R.P., Rittler J.K.;
RT "Identification of a rat oltipraz-Inducible UDP-

RT glucuronosyltransferase (UGT1A7) with activity towards benzo(a)pyrene-
RT 7,8-dihydrodiol.";
RL J. Biol. Chem. 272:1621-1627(1997).
RN [3]
RP SEQUENCE OF 1-150 FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Metz R.P., Rittler J.K.;
RL J. Biol. Chem. 0:0-0(1998).
DR EMBL: U75903; AAB18360.1; -
DR EMBL: AF039212; AAB94937.1; -
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT: 3.
KW Transferase
SQ SEQUENCE 531 AA; 59465 MW; F242D4D313B57F86 CRC64;

Query Match 1.9%; Score 10; DB 11; Length 531;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPK 365
DB 354 PONDLLGHPK 363

RESULT 18
Q46423 PRELIMINARY; PRT; 533 AA.
AC Q46423;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE.
GN UGT1A1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RA Yokota H.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB010872; BAA24692.1; -
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW Transferase
SQ SEQUENCE 533 AA; 59068 MW; B21E8361830844AE CRC64;

Query Match 1.9%; Score 10; DB 6; Length 533;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 356 PONDLLGHPK 365
DB 356 PONDLLGHPK 365

RESULT 19
Q46548 PRELIMINARY; PRT; 533 AA.
AC Q46548;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
GN UGT1A.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Court M.H.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -I- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC BETA-D-GLUCURONOSIDE.
 DR EMBL: AF039137; AAB96667.1; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UDPGT; 1.
 DR PROSITE: PS00375; UDPGT; 1.
 DR Transferrase: Glycosyltransferase.
 SQ SEQUENCE 533 AA; 58938 MW; 8FDDE2DB85F28B29 CRC64;

Query Match 1.9%; Score 10; DB 6; Length 533;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPK 365
 DB 356 PONDLLGHPK 365

RESULT 20

046549 PRELIMINARY; PRT; 533 AA.
 AC 046549;
 DT 01-JUN-1998 (TREMblrel. 06, Created)
 DT 01-JUN-1998 (TREMblrel. 06, last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
 GN UGT1A.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Court M.H.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 CC -I- CATALYTIC ACTIVITY: UDP-GLUCURONATE + ACCEPTOR = UDP + ACCEPTOR
 CC BETA-D-GLUCURONOSIDE.
 DR EMBL: AF039138; AAB96668.1; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UDPGT; 1.
 DR PROSITE: PS00375; UDPGT; 1.
 DR Transferrase: Glycosyltransferase.
 KW SEQUENCE 533 AA; 59865 MW; 94909F88EDED05F4 CRC64;

Query Match 1.9%; Score 10; DB 6; Length 533;
 Best Local Similarity 100.0%; Pred. No. 0.24;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 356 PONDLLGHPK 365
 DB 356 PONDLLGHPK 365

RESULT 21

090HH3 PRELIMINARY; PRT; 135 AA.
 AC 090HH3;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE UGT2B15 (FRAGMENT).
 GN UGT2B15.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominae; Homo.
 OX NCBI_TaxID=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Guillemette C.;
 RT "Isolation of the human UDP-glucuronosyltransferase UGT2B15
 RT promoter."
 RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF179404; AAF25010.1; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UDPGT; 1.
 DR Transferrase.
 FT NON_TER 135 135
 SQ SEQUENCE 135 AA; 15598 MW; F5F4FD9D99D4EACA CRC64;

Query Match 1.7%; Score 9; DB 4; Length 135;
 Best Local Similarity 100.0%; Pred. No. 0.73;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 RGHETVLT 57
 DB 49 RGHETVLT 57

RESULT 22

09WZ99 PRELIMINARY; PRT; 434 AA.
 AC 09WZ99;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
 DE LIPOPOLYSACCHARIDE BIOSYNTHESIS PROTEIN.
 GN TM0631.
 OS Thermotoga maritima.
 OC Bacteria; Thermotogales; Thermotoga.
 OX NCBI_TaxID=2336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MSB8 / DSM 3109;
 RX MEDLINE=99287316; PubMed=10360571;
 RA Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,
 RA Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,
 RA McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,
 RA Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,
 RA Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,
 RA Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;
 RT "Evidence for lateral gene transfer between Archaea and Bacteria from
 RT genome sequence of Thermotoga maritima."
 RL Nature 399:323-329(1999).
 DR EMBL: AE001737; AAD35715.1; -
 DR TIGR: TM0631; -
 DR InterPro: IPR001296; -
 DR Pfam: PF00534; Glycosyltransf. 1.
 SQ SEQUENCE 434 AA; 49787 MW; 49923502F59FDDDED CRC64;

Query Match 1.7%; Score 9; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 49 RGHETVLT 57
 DB 43 RGHETVLT 51

RESULT 23

091266 PRELIMINARY; PRT; 509 AA.
 AC 091266;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, last sequence update)
 DT 01-MAR-2001 (TREMblrel. 16, last annotation update)
 DE ECDYSTEROID UDP-GLUCOSYLTRANSFERASE.
 GN EGT.

OS Spodoptera litura nucleopolyhedrovirus.
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=46242;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CHINA;
 RA Martin O., Duranfel D., Croizier L., Croizier G.M.J.;
 RT "Map location, nucleotide sequence and start of transcription of the
 RT ecdysteroid UDP-glucosyltransferase of Spodoptera litura
 RT nucleopolyhedrovirus."
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: X59073; CAA67521.1; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UDPGT; 1.
 DR PROSITE: PS00375; UDPGT; 1.
 KW Transferase.
 SQ SEQUENCE 509 AA; 58495 MW; C7DA2ECA80242903 CRC64;

Query Match 1.7%; Score 9; DB 14; Length 509;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 GVPWGVPI 393
 Db 386 GVPWGVPI 394

RESULT 24
 ID 073553 PRELIMINARY; PRT; 515 AA.
 AC 073553;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE ECDYSTEROID UDP-GLUCOSYLTRANSFERASE.
 EGT.
 OS Spodoptera litoralis nuclear polyhedrosis virus (SLNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 OX NCBI_TaxID=10456;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Martin O., Smith L., Croizier L., Lopez-Ferber M., Duranfel D.,
 RA Hunter-Fujita F., Croizier G.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ003131; CAA05887.1; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UDPGT; 1.
 DR PROSITE: PS00375; UDPGT; 1.
 KW Transferase.
 SQ SEQUENCE 515 AA; 59019 MW; 37F08B6B686FB58D CRC64;

Query Match 1.7%; Score 9; DB 14; Length 515;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 385 GVPWGVPI 393
 Db 389 GVPWGVPI 397

RESULT 25
 ID 014928 PRELIMINARY; PRT; 530 AA.
 AC 014928;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 1A8.
 UG11A8.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strassburg C.P., Tukey R.H.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF030310; AAB84259.1; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UDPGT; 1.
 DR PROSITE: PS00375; UDPGT; 1.
 KW Transferase.
 SQ SEQUENCE 530 AA; 59721 MW; 98A75A1EFA2ED476 CRC64;

Query Match 1.7%; Score 9; DB 4; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
 Db 298 GIVFSLGS 306

RESULT 26
 ID 000473 PRELIMINARY; PRT; 530 AA.
 AC 000473;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 1A7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-97415544; PubMed-9271343;
 RA Strassburg C.P., Oldhafer K., Manns M.P., Tukey R.H.;
 RT "Differential expression of the UGT1A locus in human liver, biliary,
 RT and gastric tissue: identification of UGT1A7 and UGT1A10 transcripts
 RT in extrahepatic tissue."
 RL EMBL: U89507; AAB81536.1; -
 DR EMBL: U89507; AAB81536.1; -
 DR InterPro: IPR00294; -
 DR InterPro: IPR002213; -
 DR Pfam: PF00201; UDPGT; 1.
 DR PROSITE: PS00011; GLU_CARBOXYLATION; UNKNOWN_1.
 DR PROSITE: PS00375; UDPGT; 1.
 KW Transferase.
 SQ SEQUENCE 530 AA; 59774 MW; 696631BB65D3FC5C CRC64;

Query Match 1.7%; Score 9; DB 4; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
 Db 298 GIVFSLGS 306

RESULT 27
 ID 000474 PRELIMINARY; PRT; 530 AA.
 AC 000474;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 1A10.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-97415544; PubMed-9271343;
 RA Strassburg C.P., Oldhafer K., Manns M.P., Tukey R.H.;
 RT "Differential expression of the UGT1A locus in human liver, biliary,
 RT and gastric tissue: identification of UGT1A7 and UGT1A10 transcripts
 RT in extrahepatic tissue."
 RL Mol. Pharmacol. 52:212-220(1997).
 DR EMBL; U89508; AAB81537.1; -
 DR InterPro; IPR002213; -
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 DR Transferrase.
 KW
 SQ SEQUENCE 530 AA; 60037 MW; 21DB80DFBA85E177 CRC64;

Query Match 1.7%; Score 9; DB 4; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309
 |||||
 DB 298 GIVFSLGS 306

RESULT 28
 ID 060656 PRELIMINARY; PRT; 530 AA.
 AC 060656;
 DT 01-AUG-1998 (Tremblrel. 07, Created)
 DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 1A9.
 GN UGT1A9.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Ciotti M., Potter C., Owens I.S.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Owens I.S., Gong O., Cho J.W., Huang T., Potter C., Gholami N.,
 RA Basu N.K., Kubota S., Carvalho S., Pennington M.W.;
 RT "Thirteen UDP glucuronosyltransferase genes encoded at the human UGT1
 RT locus."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF056188; AAC31425.1; -
 DR EMBL; AF297093; AAC30418.1; -
 DR InterPro; IPR002213; -
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 DR Transferrase.
 KW
 SQ SEQUENCE 530 AA; 59940 MW; C417B9BE6B403078 CRC64;

Query Match 1.7%; Score 9; DB 4; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309
 |||||
 DB 298 GIVFSLGS 306

RESULT 29
 O9HAW9

ID O9HAW9 PRELIMINARY; PRT; 530 AA.
 AC O9HAW9;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 1A8.
 GN UGT1A8.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Owens I.S., Gong O., Cho J.W., Huang T., Potter C., Gholami N.,
 RA Basu N.K., Kubota S., Carvalho S., Pennington M.W.;
 RT "Thirteen UDP glucuronosyltransferase genes encoded at the human UGT1
 RT locus."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF297093; AAC30416.1; -
 DR Transferrase.
 KW
 SQ SEQUENCE 530 AA; 59741 MW; AD838436940F4190 CRC64;

Query Match 1.7%; Score 9; DB 4; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309
 |||||
 DB 298 GIVFSLGS 306

RESULT 30
 ID O9HAW8 PRELIMINARY; PRT; 530 AA.
 AC O9HAW8;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE 1A10.
 GN UGT1A10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Owens I.S., Gong O., Cho J.W., Huang T., Potter C., Gholami N.,
 RA Basu N.K., Kubota S., Carvalho S., Pennington M.W.;
 RT "Thirteen UDP glucuronosyltransferase genes encoded at the human UGT1
 RT locus."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF297093; AAC30417.1; -
 DR Transferrase.
 KW
 SQ SEQUENCE 530 AA; 59809 MW; 73774EEEC7FE37BA CRC64;

Query Match 1.7%; Score 9; DB 4; Length 530;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309
 |||||
 DB 298 GIVFSLGS 306

RESULT 31
 O9HAW7 PRELIMINARY; PRT; 530 AA.
 ID O9HAW7;
 AC O9HAW7;
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE UDP GLUCURONOSYLTRANSFERASE 1A7.
GN UGT1A7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Owens I.S., Gong Q., Cho J.W., Huang T., Potter C., Cholami N.,
BA Baas N.K., Kubota S., Carvalho S., Pennington M.W.,
RT "Thirteen UDP glucuronosyltransferase genes encoded at the human UGT1
locus".
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF297093; AAG30419.1; -
KW Transferase.
SQ SEQUENCE 530 AA; 59774 MW; DBCDA112CE27E7AB CRC64;

Query Match
Best Local Similarity 1.7%; Score 9; DB 4; Length 530;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
DB 298 GIVFSLGS 306
|||||||

RESULT 32
ID 018777 PRELIMINARY; PRT; 530 AA.
AC 018777;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 1A7 (FRAGMENT).
GN UGT1A7.
OS Oryzolaegus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA Bruck M., Li Q., Lamb J.G., Tukey R.H.,
RL Arch. Biochem. Biophys. 0:0-0(1997).
DR EMBL; AF011902; AAB65795.1; -
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
KW Transferase.
FT NON_TER 530
SQ SEQUENCE 530 AA; 60060 MW; DF98466ED57CE52D CRC64;

Query Match
Best Local Similarity 1.7%; Score 9; DB 6; Length 530;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
DB 298 GIVFSLGS 306
|||||||

RESULT 33
ID 09TSMO PRELIMINARY; PRT; 530 AA.
AC 09TSMO;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE UGT1A09.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99312152; PubMed=10385426;
RA Albert C., Vallee M., Beaudry G., Belanger A., Hum D.W.,
RT "The monkey and human uridine diphosphate-glucuronosyltransferase
RT UGT1A9, expressed in steroid target tissues, are estrogen-conjugating
RT enzymes".
RL Endocrinology 140:3292-3302(1999).
DR EMBL; AF104336; AAF15546.1; -
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
KW Transferase.
SQ SEQUENCE 530 AA; 59941 MW; EEC48F63858F3B CRC64;

Query Match
Best Local Similarity 1.7%; Score 9; DB 6; Length 530;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
DB 298 GIVFSLGS 306
|||||||

RESULT 34
ID 09TSL8 PRELIMINARY; PRT; 530 AA.
AC 09TSL8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE UGT1A08.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Albert C., Vallee M., Beaudry G., Belanger A., Hum D.W.,
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF104338; AAF15548.1; -
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
KW Transferase.
SQ SEQUENCE 530 AA; 59941 MW; F17DE1A8B1595261 CRC64;

Query Match
Best Local Similarity 1.7%; Score 9; DB 6; Length 530;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 301 GIVFSLGS 309
DB 298 GIVFSLGS 306
|||||||

RESULT 35
ID 09XS55 PRELIMINARY; PRT; 531 AA.
AC 09XS55;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE.
GN SHEUGT1A6.
OS Ovis aries (Sheep).
GN Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAFORK;
 RA MEDLINE=99208485; PubMed=10190968;
 RX Kobayashi T., Tatano A., Yokota H., Onaga T., Watanabe T., Yuasa A.;
 RT "Small intestinal UDP-glucuronosyltransferase sheUGT1A07: partial
 purification and cDNA cloning from sheep small intestine.";
 RL Arch. Biochem. Biophys. 364:143-152(1999).
 DR EMBL; AB018477; BAA77457.1; -
 DR InterPro: IPR002213; -
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW transferase.
 SQ SEQUENCE 531 AA; 60823 MW; 3AE3D0606301C1F CRC64;

Query Match 1.7%; Score 9; DB 6; Length 531;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 463 EFVMRHKGK 471
 |||||
 DB 461 EFVMRHKGK 469

RESULT 36

O9XS56 PRELIMINARY; PRT; 532 AA.
 AC O9XS56;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE.
 GN SHEUGT1A07.
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SAFORK;
 RX MEDLINE=99208485; PubMed=10190968;
 RA Kobayashi T., Tatano A., Yokota H., Onaga T., Watanabe T., Yuasa A.;
 RT "Small intestinal UDP-glucuronosyltransferase sheUGT1A07: partial
 purification and cDNA cloning from sheep small intestine.";
 RL Arch. Biochem. Biophys. 364:143-152(1999).
 DR EMBL; AB018478; BAA77458.1; -
 DR InterPro: IPR002213; -
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW transferase.
 SQ SEQUENCE 532 AA; 60718 MW; 5A21079369C25646 CRC64;

Query Match 1.7%; Score 9; DB 6; Length 532;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 463 EFVMRHKGK 471
 |||||
 DB 462 EFVMRHKGK 470

RESULT 37
 O9TSL9 PRELIMINARY; PRT; 532 AA.
 AC O9TSL9;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE UGT1A06.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecoidea; Macaca.
 CC NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Albert C., Vallee M., Beaudry G., Belanger A., Hum D.W.;
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AF104337; AAF15547.1; -
 DR InterPro: IPR002213; -
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW transferase.
 SQ SEQUENCE 532 AA; 60483 MW; 4682EFC52F1BA71 CRC64;

Query Match 1.7%; Score 9; DB 6; Length 532;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309
 |||||
 DB 300 GIVFSLGS 308

RESULT 38

O9TSL7 PRELIMINARY; PRT; 533 AA.
 AC O9TSL7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE UDP-GLUCURONOSYLTRANSFERASE UGT1A01.
 OS Macaca fascicularis (Crab eating macaque) (Cynomolus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecoidea; Macaca.
 CC NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Albert C., Vallee M., Beaudry G., Belanger A., Hum D.W.;
 RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF104339; AAF15549.1; -
 DR InterPro: IPR002213; -
 DR Pfam; PF00201; UDPGT; 1.
 DR PROSITE; PS00375; UDPGT; 1.
 KW transferase.
 SQ SEQUENCE 533 AA; 59494 MW; 601381C14BAF33E9 CRC64;

Query Match 1.7%; Score 9; DB 6; Length 533;
 Best Local Similarity 100.0%; Pred. No. 2.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 301 GIVFSLGS 309
 |||||
 DB 301 GIVFSLGS 309

RESULT 39
 O9XYN4 PRELIMINARY; PRT; 537 AA.
 AC O9XYN4;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE UDP-GLYCOSYLTRANSFERASE.
 GN UGT35A OR CG6644.
 OS Drosophila melanogaster (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
RN NCB1_TaxID=7227;
[1]
RC SEQUENCE FROM N.A.
RA STRAIN=CANTON S; TISSUE=APPENDAGE;
RW Wang Q., Hasan G., Plikielny C.;
RT "Preferential Expression of Biotransformation Enzymes in the Olfactory
Organs of Drosophila melanogaster: the Antennae.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF116555; MADS2028.1;
DR FlyBase: FBgn0026315; Ugt35a.
DR InterPro: IPR002213;
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
DR TRANSFAC:
KM SEQUENCE 537 AA; 60679 MW; 6E8523F7416189B0 CRC64;
SQ

Query Match 1.7%; Score 9; DB 5; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 RHGAKHLR 475
DB 467 RHGAKHLR 475
|||||

RESULT 40
Q9VGS9 PRELIMINARY; PRT; 537 AA.
AC Q9VGS9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE UGT35A PROTEIN.
GN UGT35A OR CG6644.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
RN NCB1_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
Buttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cateley S., Dahlke C., Davenport L.B., Davies P.,
de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merklov G., Mlshina N.V., Moberly C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
Palazzo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL: AE003690; AAF54596.1;
DR FlyBase: FBgn0026315; Ugt35a.
DR InterPro: IPR002213;
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
DR SEQUENCE 537 AA; 60733 MW; 031EC4F2F79DCD48 CRC64;
SQ

Query Match 1.7%; Score 9; DB 5; Length 537;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 RHGAKHLR 475
DB 467 RHGAKHLR 475
|||||

RESULT 41
Q9VGT8 PRELIMINARY; PRT; 559 AA.
AC Q9VGT8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE CG6633 PROTEIN.
GN UGT86DD OR CG6633.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
RN NCB1_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
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Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
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RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
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RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.",
RL Science 287:2185-2195(2000).
DR EMBL: AE003690; AAF54586.1; -
DR FlyBase: FBgn0040256; Ugt86dd.
DR InterPro: IPR002213; -
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
SO SEQUENCE 559 AA; 63722 MW; A6B30071A342395 CRC64;

Query Match 1.7%; Score 9; DB 5; Length 559;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 200 TDRMTFLER 208
DB 226 TDRMTFLER 234

RESULT 42
O9OUY6 PRELIMINARY; PRT; 17 AA.
AC O9OUY6;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE OLG0ENDOCYTE-SPECIFIC UDP-GALACTOSE: CERAMIDE GALACTOSYLTRANSFERASE
DE (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=96085162; PubMed=8521863;
RT Schulte S., Stoffel W.;
RT "UDP galactose:ceramide galactosyltransferase and glutamate/aspartate
RT transporter. Copurification, separation and characterization of the
RT two glycoproteins".
RL Eur. J. Biochem. 233:947-953(1995).
SO SEQUENCE 17 AA; 2017 MW; 0F92A645FFD7F828 CRC64;

Query Match 1.5%; Score 8; DB 11; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 356 PONDLLGH 363
DB 6 PONDLLGH 13

RESULT 43
O9OVE1 PRELIMINARY; PRT; 24 AA.
AC O9OVE1;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE BILIRUBIN UDP-GLUCURONOSYLTRANSFERASE (EC 2.4.1.17) (FRAGMENT).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;

RN [1]
RP SEQUENCE.
RX MEDLINE=92183932; PubMed=1544492;
RA Clarke D.J., Keen J.N., Burchell B.;
RT "Isolation and Characterisation of a new hepatic bilirubin UDP-
RT glucuronosyltransferase. Absence from Gunn rat liver.";
RL FEBS Lett. 299:183-186(1992).
SO SEQUENCE 24 AA; 2720 MW; 66EB29881F727872 CRC64;

Query Match 1.5%; Score 8; DB 11; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 186 PAPLSYVP 193
DB 5 PAPLSYVP 12

RESULT 44
O9HCT7 PRELIMINARY; PRT; 215 AA.
AC O9HCT7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE 2B7 (FRAGMENT).
GN UGT2B7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20242009; PubMed=10779377;
RA Ishii Y., Hansen A.J., Mackenzie P.I.;
RT "Octamer transcription factor-1 enhances hepatic nuclear factor-
RT 1alpha-mediated activation of the human UDP glucuronosyltransferase
RT 2B7 promoter.";
RL Mol. Pharmacol. 57:940-947(2000).
DR EMBL: AF282881; AAC01472.1; -
KW Transferase.
FT NON_TER 215
SO SEQUENCE 215 AA; 24789 MW; B77AC742E46D6826 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 215;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 RGHEVTVL 56
DB 49 RGHEVTVL 56

RESULT 45
O9H3G2 PRELIMINARY; PRT; 284 AA.
AC O9H3G2;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE UDP-GLUCURONOSYLTRANSFERASE (FRAGMENT).
GN UGT1A7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Guillemette C.;
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF110191; AAG43194.1; -

KW Transferrase. 284
 FT NON_TER 284
 SQ SEQUENCE 284 AA; 32392 MW; B30DA3706B42F8D9 CRC64;

Query Match 1.58; Score 8; DB 4; Length 284;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 186 PAPLSYVP 193
 Db 184 PAPLSYVP 191

Search completed: August 13, 2001, 13:47:01
 Job time: 201 sec